



Letter to the Editor

Severe fever with thrombocytopenia syndrome bunyavirus (SFTSV) infections in Zhejiang Province, China

Bunyaviruses are becoming increasingly important as ecological changes modulate vector dynamics and humans become targets.^{1,2} A novel Phlebovirus in the *Bunyaviridae* family, designated as severe fever with thrombocytopenia syndrome bunyavirus (SFTSV), was confirmed to be associated with the SFTS reported in rural areas of Hubei and Henan provinces in central China.³ Sporadic cases infected by SFTSV have also been found in other non-epidemic regions of China.⁴ According to recent studies, SFTSV can be transmitted from person to person through blood contact.^{5,6} As a result, enhanced surveillance has been implemented for the effective control and prevention of SFTSV infections in epidemic regions.

During these years, patients with hemorrhagic fever-like illnesses of unknown etiology have also been found in Zhejiang Province, which borders the epidemic regions for SFTS disease (Anhui and Jiangsu). However, infections of SFTSV in Zhejiang Province have not been investigated before. In this study, blood specimens were collected from suspected patients during the acute phase, and serum samples were used for SFTSV detection. In accordance with the diagnostic criteria, SFTSV RNA was detected through real-time reverse transcriptase PCR (RT-PCR).⁷

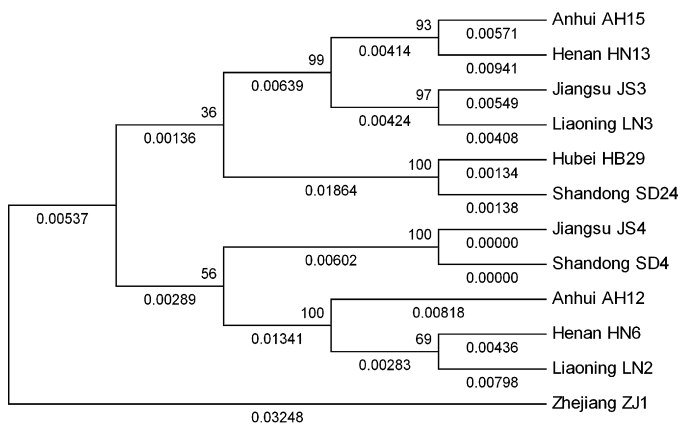


Figure 1. Phylogenetic analysis of the SFTSV Bunyavirus isolates. The phylogenetic tree shown was generated using Mega 4.0 software from aligned nucleocapsid gene sequences of the SFTSV isolates, including strains from Zhejiang and a further six established epidemic regions. Gene comparison was analyzed with the neighbor-joining method; bootstrap testing was also performed and the bootstrap values are indicated.

Positive serum samples were inoculated into Vero cells for SFTSV isolation.

Samples from 30 suspected cases were subjected to RT-PCR for the detection of SFTSV RNA and 12 cases were identified as SFTSV infection. SFTSV was isolated and successfully cultured, and a phylogenetic analysis was performed based on the nucleocapsid gene sequence (Figure 1). Results showed 88.1% identical ratios of all the nucleocapsid gene sequences from the different isolates. From the phylogenetic tree, it is interesting to observe that the SFTSV isolates from Zhejiang are present in an independent branch to that of the isolates from the epidemic regions.

In this study, symptom onset among patients with confirmed or clinically diagnosed SFTSV occurred mainly from May to July. All age groups were affected, but most infections occurred among persons over 50 years of age; nine (75%) were women, and almost all the patients were peasants.

This is the first time that SFTSV has been detected in Zhejiang Province, East China. It is also the first time that SFTSV infections have been found in insular areas. SFTSV could be an important cause of the hemorrhagic fever-like disease here. Clinical vigilance and strong epidemiologic and laboratory surveillance are essential for the control of this disease in Zhejiang.

Acknowledgements

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Conflict of interest: We declare that we have no competing interests.

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